Supplementary Online Content

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This supplementary material has been provided by the authors to give readers additional information about their work.

eTable 1. ICD-10 and ICD-9 Codes for Cirrhosis, Decompensated Cirrhosis, and HCC

Diagnosis	ICD9		ICD10
	.== -		
HEPATOCELLULAR CARCINOMA	155.0	HEPATOCELLULAR CARCINOMA	C22.0
CIRRHOSIS			
Alcoholic Cirrhosis Of Liver	571.2	Alcoholic cirrhosis without ascites	K70.30
Cirrhosis Of Liver Without Mention Of	571.5	Other cirrhosis of liver	K74.69
Alcohol			
		Unspecified cirrhosis of the liver	K74.60
		Pigmentary cirrhosis of the liver	E83.110
		Cirrhosis (of liver) with toxic liver disease	K71.7
DECOMPENSATED CIRRHOSIS			
(INCLUDES ANY OF THE FOLLOWING)			
VARICES NO BLEEDING			
Esophageal Varices Without Mention Of Bleeding	456.1	Esophageal varices, no bleeding	185.00
Esophageal Varices In Diseases Classified Elsewhere, Without Mention Of Bleeding	456.21	Gastric Varices, no bleeding	186.40
		Secondary esophageal varices, no bleeding	I85.10
VARICES WITH BLEEDING		,	
Esophageal Varices With Bleeding	456.0	Esophageal varices, with bleeding	I85.01
Esophageal Varices In Diseases Classified Elsewhere, With Bleeding	456.20	Gastric Varices, with bleeding	186.41
		Secondary esophageal varices, with bleeding	I85.11
ASCITES			
Ascites	789.5	Alcoholic cirrhosis with ascites	K70.31
Other ascites	789.60	Ascites in alcoholic hepatitis	K70.11
Non-malignant ascites	789.59	Ascites in toxic liver disease with chronic active hepatitis	K71.51
		Other ascites	R18.8
SPONTANEOUS BACTERIAL PERITONITIS	567.23		K65.2
ENCEPHALOPATHY*			
Encephalopathy	572.2	Hepatic failure, unspecified with coma	K72.91
Chronic hepatitis C with hepatic coma		Encephalopathy, unspecified	G93.40
		Chronic failure with coma	K72.11
HEPATORENAL SYNDROME	572.5		K76.7
HEPATOPULMONARY SYNDROME	573.5		K76.81

eTable 2. Feature Selection Frequency Over 10 Splits for the Longitudinal LR With Lasso Penalty¹

Feature	Selection	Feature	Selection	Feature	Selection
	frequency		frequency	have a state in the state of th	frequency
genotype_main_>=4	10	alkalinephosphatase_max	10	hemoglobin_maxdiff	9
alt_maxdiff	10	alkalinephosphatase_min	10	totprotein_max	9
potassium_tv	10	alkalinephosphatase_min diff	10	ASTALT_min	9
glucose_max	10	alkalinephosphatase_max diff 10 albumin_tv		9	
glucose_min	10	APRI_min	10	alkalinephosphataseratio_min	9
glucose_tv	10	APRI_tv	10	wbc_tv	9
plt_max	10	hemoglobin_tv	10	alphafetoprotein_mindiff	9
plt_min	10	sodium_max	10	Fib4_min	9
plt_mindiff	10	BMI_tv	10	alphafetoproteinratio_min	9
alt_max	10	inr_mindiff	10	bilirubin_max	9
alt mindiff	10	Race_HISPANIC	10	Race WHITE	9
alphafetoprotein max	10	bilirubin mindiff	10	glucose_mindiff	8
potassium_mindiff	10	Race_BLACK OR AFRICAN AMERICAN	10		
alphafetoprotein_maxdi ff	10	inr_max			8
genotype_main_3	10	AgeAtCirrhosis	10	APRI_max	8
bloodureanitro max	10	inr min	10	totprotein_maxdiff	8
bloodureanitro_min	10	SVR	10	Fib4_maxdiff	8
bloodureanitro_mindiff	10	BMI_maxdiff	10	inr_maxdiff	8
bloodureanitro_maxdiff	10	albumin_maxdiff	10	alkalinephosphataseratio ma	
hemoglobin_max	10	albumin min	10	alphafetoproteinratio_maxdiff	8
hemoglobin min	10	albumin max	10	alkalinephosphatase_tv	7
hemoglobin_mindiff	10			APRI mindiff	7
potassium_maxdiff	10	wbc min			7
potassium_min	10	wbc_maxdiff			7
ASTALT_tv	10	Race_OTHER	alkalinenhosphata		7
chloride mindiff	10	bilirubin_tv	10	alt_min	7
sodium min	10	genotype_main_2	10	ast mindiff	7
sodium mindiff	10	Gender_M	10	plt tv	6
sodium maxdiff	10	BMI_min	10	alphafetoprotein min	6
sodium tv	10	ast_min	10	bilirubin min	6
Fib4 max	10	BMI_max	10	astratio_maxdiff	6
creatinine_max	10	ast_tv	10	BMI mindiff	6
creatinine_min	10	genotype_main_1	10	creatinine tv	6
chloride max	10	ast maxdiff	10	inr_tv	6
chloride_min	10	ast_max	10	ASTALT max	6
chloride maxdiff	10	Gender F	10	altratio max	6
potassium_max	10	totprotein_mindiff	10		
totprotein_min	10	totprotein tv	10		
-		· —		l 27 features were calcuted for	I

¹For two logistic regression models with feature selection, 36 out of the original 37 features were selected for the cross-sectional-LR and 112 out of the original 137 features were selected for the longitudinal-LR. The prediction performance

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of two logistic regression models with lasso penalty is very close to that of models without lasso penalty - the average AUROC, AUPRC and Brier score of the longitudinal-LR were 0.689, 0.353 and 0.149; those of the cross-sectional-LR were 0.682, 0.344 and 0.150. The RNN model achieved better prediction performance than two logistic regression models either with feature selection or without feature selection.

eTable 3. Comparison of the Performance Characteristics of 3 Different Models Predicting the Development of HCC Within 3 years in Male Patients with HCV-Related Cirrhosis

MALE PATIENTS	Cross-sectional LR Model	Longitudinal LR Model	RNN Model	P-value compared to RNN model
AUROC	0.681±0.008	0.688±0.010	0.757±0.009	<0.0001
Brier score	0.151±0.003	0.150±0.003	0.137±0.003	<0.0001
AUPRC	0.346±0.011	0.362±0.009	0.481±0.019	<0.0001
Proportion of patients who test positive at 90% sensitivity	0.749±0.007	0.739±0.013	0.667±0.012	<0.0001
Specificity at 90% sensitivity	0.289 <u>+</u> 0.009	0.302±0.016	0.392 <u>+</u> 0.014	<0.0001
Positive predictive value at 90% sensitivity	0.244±0.006	0.248±0.007	0.274±0.005	<0.0001
Negative predictive value at 90% sensitivity	0.918±0.003	0.921±0.004	0.938±0.003	<0.0001
Proportion of patients who test positive at 80% sensitivity	0.602±0.012	0.594±0.017	0.515±0.016	<0.0001
Specificity at 80% sensitivity	0.447±0.015	0.458±0.021	0.558±0.019	<0.0001
Positive predictive value at 80% sensitivity	0.270±0.007	0.274±0.009	0.3165±0.010	<0.0001
Negative predictive value at 80% sensitivity	0.897±0.005	0.899±0.005	0.916±0.004	<0.0001